

CLAIMS

1. A method of producing a transgenic plant which harbours within the genome of the plant a chimaeric gene, the expression of which gene causes plant cytotoxicity at a target site, wherein a plant is transformed with a chimaeric gene comprising a promoter, which promoter is induced at and/or adjacent to a target site, operably linked to a coding sequence, which coding sequence encodes a maize ribosome inactivating protein or a part thereof.
2. A method of producing a transgenic plant according to Claim 1, wherein the coding sequence of said maize ribosome inactivating protein comprises a pro-maize ribosome inactivating protein comprising the N-terminal, the α domain, the central spacer peptide, the β domain and the C-terminal peptide.
3. A method of producing a transgenic plant according to Claim 1, wherein the coding sequence of said maize ribosome inactivating protein comprises a recombinant mature RIP comprising an α domain and a β domain arranged contiguously.
4. A method of producing a transgenic plant according to Claim 1, wherein the coding sequence of said maize ribosome inactivating protein comprises a recombinant RIP

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comprising as the active part the α domain only of a maize ribosome inactivating protein.

5. A method of producing a transformed plant according to Claim 1, wherein the coding sequence of said ribosome inactivating protein comprises as the active part a recombinant RIP comprising the β domain only of a maize ribosome inactivating protein.
6. A method of producing a transformed plant according to Claims 1 or 2, wherein said coding sequence comprises the coding sequence identified as SEQ. ID. No.: 1, or a coding sequence which is homologous thereto.
7. A method of producing a transformed plant according to Claims 1 or 3, wherein said coding sequence comprises the sequence identified in SEQ. ID. No.: 2 or a coding sequence which is homologous thereto.
8. A method of producing a transformed plant according to Claim 4, wherein said coding sequence comprises the sequence identified in SEQ. ID. No.: 3 or a coding sequence homologous thereto.
9. A method of producing a transformed plant according to Claim 5, wherein said coding sequence comprises the sequence identified in SEQ. ID. No.: 4 or a coding sequence homologous thereto.
10. A method of producing a transformed plant according to Claims 6, 7, 8 or 9, wherein said homologous coding

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sequence has at least 70% with SEQ. ID. No.: 1; SEQ. ID. No.: 2; SEQ. ID. No.: 3; or SEQ. ID. No.: 4; respectively.

11. A method of producing a transformed plant according to Claim 10, wherein said homologous coding sequence has at least 80% homology with SEQ. ID. No.: 1; SEQ. ID. No.: 2; SEQ. ID. No.: 3; or SEQ. ID. No.: 4; respectively.
12. A method of producing a transformed plant according to Claim 10 or 11, wherein said homologous coding sequence has at least 85% homology with SEQ. ID. No.: 1; SEQ. ID. No.: 2; SEQ. ID. No.: 3; or SEQ. ID. No.: 4; respectively.
13. A method of producing a transformed plant according to Claim 10, 11 or 12, wherein said homologous coding sequence has at least 90% homology with SEQ. ID. No.: 1; SEQ. ID. No.: 2; SEQ. ID. No.: 3; or SEQ. ID. No.: 4; respectively.
14. A method of producing a transformed plant according to any one of the preceding claims, wherein said chimaeric gene further comprises a 3' untranslated terminator sequence.
15. A method of producing a transformed plant according to Claim 14, wherein said 3' untranslated terminator sequence is from plant, bacterial or viral genes.

16. A method of producing a transformed plant according to any one of Claims 14 or 15, wherein said 3' untranslated terminator sequence is selected from the group comprising the pea *rbcS* E9 terminator sequence, the *nos* terminator sequence derived from the nopaline synthase gene of *Agrobacterium tumefaciens* and the 35S terminator sequence from cauliflower mosaic virus.
17. A method of producing a transformed plant according to any one of the preceding claims, wherein said chimaeric gene comprises a transcriptional or translational enhancer sequence and/or intracellular targeting sequences and introns, and/or nucleotide sequences operable to facilitate the transformation process and the stable expression of said chimaeric gene.
18. A method of producing a transformed plant according to any one of the preceding claims, wherein said chimaeric gene comprises a first promoter operably linked to an α domain of a maize ribosome inhibiting protein and a second promoter operably linked to a β domain of a maize ribosome inhibiting promoter.
19. A method according to Claim 18, wherein said first and second promoters express at one overlapping target site.
20. A method according to Claim 18 or 19, wherein said first promoter is the KNT1 promoter and the second promoter is the KNT2 promoter (SEQ. ID. No.: 18).

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25. A DNA isolate of a chimaeric gene according to Claim 24, said first and second promoters having one overlapping expression site.
26. A biologically functional expression vehicle containing a chimaeric gene comprising a promoter, which promoter is induced at and/or adjacent to a target site, operably linked to a coding sequence, which coding sequence encodes a maize ribosome inactivating protein or a part thereof.
27. A biologically functional expression vehicle according to Claim 26, said expression vehicle further comprising a first promoter operably linked to a first domain of a maize ribosome inactivating protein and a second promoter operably linked to a second domain of a maize ribosome inactivating protein.

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